

0590

04/18



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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/068,486A

DATE: 04/18/2003

TIME: 16:00:15

Input Set : A:\GA0217C.ST25.txt

Output Set: N:\CRF4\04182003\J068486A.raw

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3 <110> APPLICANT: Genzyme Corporation
4      Nacht, Mariana
6 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CLAUDIN-7
8 <130> FILE REFERENCE: GA0217C
10 <140> CURRENT APPLICATION NUMBER: US 10/068,486A
11 <141> CURRENT FILING DATE: 2002-02-05
13 <150> PRIOR APPLICATION NUMBER: PCT/US00/24174
14 <151> PRIOR FILING DATE: 2000-08-07
16 <150> PRIOR APPLICATION NUMBER: US 60/147,752
17 <151> PRIOR FILING DATE: 1999-08-06
19 <160> NUMBER OF SEQ ID NOS: 2
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 681
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (40)..(672)
31 <223> OTHER INFORMATION:
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35                                     Met Ala Asn Trp Gly
36                                     1      5
38 ctg cag ttg ctg ggc ttc tcc atg gcc ctg ctg ggc tgg gtg ggt ctg      102
39 Leu Gln Leu Leu Gly Phe Ser Met Ala Leu Leu Gly Trp Val Gly Leu
40                                     10      15      20
42 gtg gcc tgc acc gcc atc ccg cag tgg cag atg agc tcc tat gcg ggt      150
43 Val Ala Cys Thr Ala Ile Pro Gln Trp Gln Met Ser Ser Tyr Ala Gly
44                                     25      30      35
46 gac aac atc atc acg gcc cag gcc atg tac aag ggg ctg tgg atg gac      198
47 Asp Asn Ile Ile Thr Ala Gln Ala Met Tyr Lys Gly Leu Trp Met Asp
48                                     40      45      50
50 tgc gtc acg cag agc acg ggg atg atg agc tgc aaa atg tac gac tcg      246
51 Cys Val Thr Gln Ser Thr Gly Met Met Ser Cys Lys Met Tyr Asp Ser
52                                     55      60      65
54 gtg ctc gcc ctg tcc gcg gcc ttg cag gcc act cga gcc cta atg gtg      294
55 Val Leu Ala Leu Ser Ala Ala Leu Gln Ala Thr Arg Ala Leu Met Val
56 70                                     75      80      85
58 gtc tcc ctg gtg ctg ggc ttc ctg gcc atg ttt gtg gcc acg atg ggc      342
59 Val Ser Leu Val Leu Gly Phe Leu Ala Met Phe Val Ala Thr Met Gly
60                                     90      95      100
62 atg aag tgc acg cgc tgt ggg gga gac gac aaa gtg aag aag gcc cgt      390

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63 Met Lys Cys Thr Arg Cys Gly Gly Asp Asp Lys Val Lys Lys Ala Arg
64          105          110          115
66 ata gcc atg ggt gga ggc ata att ttc atc gtg gca ggt ctt gcc gcc      438
67 Ile Ala Met Gly Gly Gly Ile Ile Phe Ile Val Ala Gly Leu Ala Ala
68          120          125          130
70 ttg gta gct tgc tcc tgg tat ggc cat cag att gtc aca gac ttt tat      486
71 Leu Val Ala Cys Ser Trp Tyr Gly His Gln Ile Val Thr Asp Phe Tyr
72          135          140          145
74 aac cct ttg atc cct acc aac att aag tat gag ttt ggc cct gcc atc      534
75 Asn Pro Leu Ile Pro Thr Asn Ile Lys Tyr Glu Phe Gly Pro Ala Ile
76 150          155          160          165
78 ttt att ggc tgg gca ggg tct gcc cta gtc atc ctg gga ggt gca ctg      582
79 Phe Ile Gly Trp Ala Gly Ser Ala Leu Val Ile Leu Gly Gly Ala Leu
80          170          175          180
82 ctc tcc tgt tcc tgt cct ggg aat gag agc aag gct ggg tac cgt gca      630
83 Leu Ser Cys Ser Cys Pro Gly Asn Glu Ser Lys Ala Gly Tyr Arg Ala
84          185          190          195
86 ccc cgc tct tac cct aag tcc aac tct tcc aag gag tat gtg tgagtcgac      681
87 Pro Arg Ser Tyr Pro Lys Ser Asn Ser Ser Lys Glu Tyr Val
88          200          205          210
91 <210> SEQ ID NO: 2
92 <211> LENGTH: 211
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo sapiens
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103          20          25          30
106 Ser Ser Tyr Ala Gly Asp Asn Ile Ile Thr Ala Gln Ala Met Tyr Lys
107          35          40          45
110 Gly Leu Trp Met Asp Cys Val Thr Gln Ser Thr Gly Met Met Ser Cys
111          50          55          60
114 Lys Met Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala Leu Gln Ala Thr
115 65          70          75          80
118 Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe Leu Ala Met Phe
119          85          90          95
122 Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly Gly Asp Asp Lys
123          100          105          110
126 Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile Ile Phe Ile Val
127          115          120          125
130 Ala Gly Leu Ala Ala Leu Val Ala Cys Ser Trp Tyr Gly His Gln Ile
131          130          135          140
134 Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn Ile Lys Tyr Glu
135 145          150          155          160
138 Phe Gly Pro Ala Ile Phe Ile Gly Trp Ala Gly Ser Ala Leu Val Ile
139          165          170          175
142 Leu Gly Gly Ala Leu Leu Ser Cys Ser Cys Pro Gly Asn Glu Ser Lys
143          180          185          190

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146	Ala	Gly	Tyr	Arg	Ala	Pro	Arg	Ser	Tyr	Pro	Lys	Ser	Asn	Ser	Ser	Lys
147			195					200					205			
150	Glu	Tyr	Val													
151		210														

**VERIFICATION SUMMARY**

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